



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 154530

TO: Brian Kwon
Location: REM-3A74/3C70
Art Unit: 1614
Friday, May 27, 2005

Case Serial Number: 09/763616

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

RUSH

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"Rush"

Access DB#

154530

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Brian Kwon Examiner #: 78155 Date: 5/26/05
An Unit: 1614 Phone Number 30 _____ Serial Number: 69/262616
Mail Box and Bldg/Room Location: 3A74 Results Format Preferred (circle): PAPER DISK E-MAIL
remson 303CM

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: therapeutic compounds and methods
Inventors (please provide full names): _____

Earliest Priority Filing Date: 7/15/99

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

RECEIVED
MAY 26 2005
STIC
Sequence search for claim 32
~~_____~~

please search commercial data base as well as
Interference Search

Thank

Rush Search
Approved

STAFF USE ONLY
Searcher: POB Type of Search _____ Vendors and cost where applicable _____
NA Sequence (#) _____ STN _____
AA Sequence (#) 1 _____
Source Phone # _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 00:22:40 ; Search time 161 Seconds
(without alignments)
88.883 Million cell updates/sec

Title: US-09-763-616-2

Perfect score: 69
Sequence: 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	37	3	Aay82461 Chelated
2	69	100.0	37	3	Aay91614 Human sec
3	69	100.0	37	8	ADL71690 Novel hum
4	69	100.0	46	3	AAG56091 Arabidops
5	69	100.0	47	8	ABO59388 Human gen
6	69	100.0	50	4	AAM13839 Peptide #
7	69	100.0	50	4	ABB32784 Peptide #
8	69	100.0	50	4	AAM26246 Peptide #
9	69	100.0	50	4	ABB27614 Human pep
10	69	100.0	50	4	ABB18267 Protein #
11	69	100.0	50	4	AAM55971 Human bon
12	69	100.0	50	4	AAM53591 Human bra
13	69	100.0	50	4	ABG47636 Human liv
14	69	100.0	50	4	AAM01583 Peptide #
15	69	100.0	50	5	ABG35618 Human pep
16	69	100.0	50	6	AAM016632 Human pap
17	69	100.0	52	3	AAY96950 Rubredoxi
18	69	100.0	53	6	ABR63889
19	69	100.0	53	8	ADN46935 Thermococ
20	69	100.0	54	1	AAP92305 Sequence
21	69	100.0	54	8	ABO60186 Human gen
22	69	100.0	55	4	ABB65559 Drosophil
23	69	100.0	55	6	ABP99543 An epitop
24	69	100.0	56	4	ABB66566 Drosophil
25	69	100.0	58	5	ABP09095 Human ORF

26	69	100.0	59	8	ADN46780	Adn46780 Thermococ
27	69	100.0	60	4	AAM15683	Aam15683 Peptide #
28	69	100.0	60	4	AAM28187	Aam28187 Peptide #
29	69	100.0	60	4	ABB20093	Abb20093 Protein #
30	69	100.0	60	4	AAM03419	Aam03419 Peptide #
31	69	100.0	60	5	ABG37409	Abg37409 Human pep
32	69	100.0	61	4	AU39623	Aau39623 Propionib
33	69	100.0	61	4	ABG23599	Abg23599 Novel hum
34	69	100.0	61	6	ABM36142	Abm36142 Propionib
35	69	100.0	62	8	ADP31006	Adp31006 Human sec
36	69	100.0	63	4	AAM15926	Aam15926 Peptide #
37	69	100.0	63	4	ABB66560	Abb66560 Drosophil
38	69	100.0	63	4	ABB34913	Abb34913 Peptide #
39	69	100.0	63	4	AAM28429	Aam28429 Peptide #
40	69	100.0	63	4	ABB29742	Abb29742 Peptide #
41	69	100.0	63	4	ABB20327	Abb20327 Protein #
42	69	100.0	63	4	AAM68102	Aam68102 Human bon
43	69	100.0	63	4	AAM55724	Aam55724 Human bra
44	69	100.0	63	4	ABG49752	Abg49752 Human liv
45	69	100.0	63	4	AAM03662	Aam03662 Peptide #

ALIGNMENTS

RESULT 1
AAY82461
ID AAY82461 standard; peptide; 37 AA.

AC AAY82461;

DT 30-JUN-2000 (first entry)

DE Chelated zinc domain sequence motif.

XX Chelated zinc finger; therapeutic; treatment; prophylaxis; MPV;
XX mammalian papillomavirus; antiviral; cytostatic; cervical cancer; lesion;
XX wart.

OS Unidentified.

XX Key Location/Qualifiers
FT Misc-difference 2 /note= "unspecified"
FT Misc-difference 3 /note= "unspecified"
FT Misc-difference 5 /note= "unspecified"
FT Misc-difference 6 /note= "unspecified"
FT Misc-difference 7 /note= "unspecified"
FT Misc-difference 8 /note= "unspecified"
FT Misc-difference 9 /note= "unspecified"
FT Misc-difference 10 /note= "unspecified"
FT Misc-difference 11 /note= "unspecified"
FT Misc-difference 12 /note= "unspecified"
FT Misc-difference 13 /note= "unspecified"
FT Misc-difference 14 /note= "unspecified"
FT Misc-difference 15 /note= "unspecified"
FT Misc-difference 16 /note= "unspecified"
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FT Misc-difference 18 /note= "unspecified"

FT Misc-difference 19 /note= "unspecified"
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FT Misc-difference 21 /note= "unspecified"
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FT Misc-difference 26 /note= "unspecified"
FT Misc-difference 27 /note= "unspecified"
FT Misc-difference 28 /note= "unspecified"
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FT Misc-difference 31 /note= "unspecified"
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FT Misc-difference 33 /note= "unspecified"
FT Misc-difference 35 /note= "unspecified"
FT Misc-difference 36 /note= "unspecified"
XX W0200014063-A1.
XX
XX PD 16-MAR-2000.
XX PF 03-SEP-1999; 99WO-AU000724.
XX PR 04-SEP-1998; 98AU-00005733.
XX PR 15-JUL-1999; 99AU-00001645.
XX (MOLE-) INST MOLECULAR & CELL BIOLOGY.
XX PA (HUGH/) HUGHES E J L.
XX PI Bernard H, Tan YJ, Beerheide W, Ting AE, Sim MM;
XX WPI; 2000-256917/22.
XX
XX Polysulfide and dithionodisulfide agents, useful for the treatment or prophylaxis of diseases caused by mammalian papillomavirus, are disruptors of a chelated metal cation domain in an MPV gene encoded protein.
XX
XX Claim 9; Page 50; 78pp; English.
XX
XX The present invention describes an agent used in the treatment or prophylaxis of a disease caused or exacerbated by MPV (mammalian papillomavirus) comprising a compound capable of reducing, inhibiting or otherwise decreasing the activity of a protein encoded by an MPV gene by facilitating disruption of a chelated metal cation domain present in the protein. An agent of the present invention can be used to treat cervical cancer or its HPV associated precursor lesions or other HPV associated cancers and/or warts. The present sequence represents a specifically claimed conserved motif sequence for a chelated zinc domain
XX
XX Sequence 37 AA;

Query Match 100.0%; Score 69; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
RESULT 2
AAAY91614
ID AAAY91614 standard; protein; 37 AA.
XX
AC AAAY91614;
XX
XX 29-JUN-2000 (first entry)
XX Human secreted protein sequence encoded by gene 17 SEQ ID NO:287.
XX
XX Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW antiHIV; antiinflammatory; nontropic; neuroprotective; antiallergic;
KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
KW immune disease; inflammation; blood disorder; tumour.
XX
XX Homo sapiens.
XX
XX W0200006698-A1.
XX
XX 10-FEB-2000.
XX
XX 29-JUL-1999; 99WO-US017130.
XX
XX 30-JUL-1998; 98US-0094657P.
PR 05-AUG-1998; 98US-0095486P.
PR 06-AUG-1998; 98US-0095454P.
PR 06-AUG-1998; 98US-0095455P.
PR 12-AUG-1998; 98US-0096319P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX
XX WPI; 2000-195282/17.
XX
XX New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
XX
XX Disclosure; Page 48; 634pp; English.
XX
XX The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAAY91451 to AAAY91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic; immunosuppressive; antiHIV; antiinflammatory; nontropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides. Based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, Alzheimer's and behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, CC

DR WPI; 2004-180094/17.

PR 01-APR-1999; 99US-0127462P;
PR 05-APR-1999; 99US-0128234P

PR 01-APR-1999; 99US-0127462P;
PR 05-APR-1999; 99US-0128234P

PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130049P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131149P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 25-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
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PR 22-JUN-1999; 99US-0139817P.
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PR 28-JUN-1999; 99US-0140823P.
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PR 01-JUL-1999; 99US-0141842P.
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PR 15-JUL-1999; 99US-0144005P.
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PR 19-JUL-1999; 99US-0144332P.

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PR 21-JUL-1999; 99US-0145086P.
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PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
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PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 06-OCT-1999; 99US-0157753P.
PR 07-OCT-1999; 99US-0157865P.
PR 08-OCT-1999; 99US-0158029P.
PR 12-OCT-1999; 99US-0158232P.
PR 13-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488901/53.
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human cervical epithelial cells.
 PT Claim 27; SEQ ID NO 18665; 487pp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENP; see AAI10068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 50 AA;
 SQ
 Query Match 100.0%; Score 69; DB 4; Length 50;
 Best Local Similarity 10.8%; Pred. No. 1e+03;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
 Db 11 CIRCCGVHVSRLTHSRNIRIGLIRSECLC 47
 RESULT 7
 ABB32784
 ID ABB32784 standard; peptide; 50 AA.
 XX
 AC ABB32784;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #290 encoded by human foetal liver single exon probe.
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.
 KW Homo sapiens.
 OS
 XX WO200157277-A2.
 PN
 XX 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000669.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human fetal liver.

XX Claim 27; SEQ ID NO 25419; 639pp + Sequence Listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 50 AA;
 SQ
 Query Match 100.0%; Score 69; DB 4; Length 50;
 Best Local Similarity 10.8%; Pred. No. 1e+03;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
 Db 11 CIRCCGVHVSRLTHSRNIRIGLIRSECLC 47
 RESULT 8
 AAM26246
 ID AAM26246 standard; protein; 50 AA.
 XX
 AC AAM26246;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #283 encoded by probe for measuring placental gene expression.
 XX Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 OS Homo sapiens.
 XX WO200157272-A2.
 PN
 XX 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000663.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human placenta.
 XX Claim 27; SEQ ID NO 26515; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP;
 CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XX Sequence 50 AA;
 SQ
 Query Match 100.0%; Score 69; DB 4; Length 50;


```
ID  AAM65971 standard; protein; 50 AA.
XX
AC  AAM65971;
XX
DT  06-NOV-2001 (first entry)
XX
DE  Human bone marrow expressed probe encoded protein SEQ ID NO: 26277.
XX
KW  Human; bone marrow expressed exon; gene expression analysis; probe;
XX  microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS  Homo sapiens.
XX
PN  WO200157276-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US000668.
XX
PR  04-FEB-2000; 2000US-0180312P.
XX  26-MAY-2000; 2000US-0207456P.
XX  30-JUN-2000; 2000US-00608408.
XX  03-AUG-2000; 2000US-00632366.
XX  21-SEP-2000; 2000US-0234687P.
XX  27-SEP-2000; 2000US-0236359P.
XX  04-OCT-2000; 2000GB-00024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR  WPI; 2001-488900/53.
XX
PT  Human genome-derived single exon nucleic acid probes useful for analyzing
XX  gene expression in human bone marrow.
XX
PS  Example 4; SEQ ID NO 26277; 658pp + Sequence Listing; English.
XX
CC  The present invention provides a number of single exon nucleic acid
XX  probes which are derived from genomic sequences expressed in the human
XX  bone marrow. They can be used to measure gene expression in bone marrow
XX  samples, which may enable the improved diagnosis and treatment of cancers
XX  such as lymphoma, leukaemia and myeloma. The present sequence is a
XX  protein encoded by one of the probes of the invention
XX
SQ  Sequence 50 AA;

Query Match      100.0%; Score 69; DB 4; Length 50;
Best Local Similarity 10.8%; Pred. No. 1e+03;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db  11 CIRCCGSHVQSHSLTHSRNSIRIGRLIRSECLEC 47

RESULT 12
AAM53591
ID  AAM53591 standard; protein; 50 AA.
XX
AC  AAM53591;
XX
DT  05-NOV-2001 (first entry)
XX
DE  Human brain expressed single exon probe encoded protein SEQ ID NO: 25696.
XX
KW  Human; brain expressed exon; gene expression analysis; probe; microarray;
XX  Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS  Homo sapiens.
XX
PN  WO200157275-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US000664.
XX
PR  04-FEB-2000; 2000US-0180312P.
XX  26-MAY-2000; 2000US-0207456P.
XX  30-JUN-2000; 2000US-00608408.
XX  03-AUG-2000; 2000US-00632366.
XX  21-SEP-2000; 2000US-0234687P.
XX  27-SEP-2000; 2000US-0236359P.
XX  04-OCT-2000; 2000GB-00024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR  WPI; 2001-488900/53.
XX
PT  Human genome-derived single exon nucleic acid probes useful for analyzing
XX  gene expression in human bone marrow.
XX
PS  Example 4; SEQ ID NO 26277; 658pp + Sequence Listing; English.
XX
CC  The present invention provides a number of single exon nucleic acid
XX  probes which are derived from genomic sequences expressed in the human
XX  bone marrow. They can be used to measure gene expression in bone marrow
XX  samples, which may enable the improved diagnosis and treatment of cancers
XX  such as lymphoma, leukaemia and myeloma. The present sequence is a
XX  protein encoded by one of the probes of the invention
XX
SQ  Sequence 50 AA;

Query Match      100.0%; Score 69; DB 4; Length 50;
Best Local Similarity 10.8%; Pred. No. 1e+03;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db  11 CIRCCGSHVQSHSLTHSRNSIRIGRLIRSECLEC 47

RESULT 13
ABG47636
ID  ABG47636 standard; peptide; 50 AA.
XX
AC  ABG47636;
XX
DT  25-FEB-2003 (first entry)
XX
DE  Human liver peptide, SEQ ID No 26284.
XX
KW  Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX  hypercholesterolaemia; coronary heart disease.
XX
OS  Homo sapiens.
XX
PN  WO200157273-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US000664.
XX
PR  04-FEB-2000; 2000US-0180312P.
XX  26-MAY-2000; 2000US-0207456P.
XX  30-JUN-2000; 2000US-00608408.
XX  03-AUG-2000; 2000US-00632366.
XX  21-SEP-2000; 2000US-0234687P.
XX  27-SEP-2000; 2000US-0236359P.
XX  04-OCT-2000; 2000GB-00024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR  WPI; 2001-483446/52.
XX
PT  Single exon nucleic acid probes for analyzing gene expression in human
XX  brains.
XX
PS  Example 4; SEQ ID NO 25696; 650pp + Sequence Listing; English.
XX
CC  The present invention provides a number of single exon nucleic acid
XX  probes which are derived from genomic sequences expressed in the human
XX  brain. They can be used to measure gene expression in brain cell samples,
XX  which may enable the diagnosis and improved treatment of nervous system
XX  diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX  epilepsy and cancers. The present sequence is a protein encoded by one of
XX  the probes of the invention
XX
SQ  Sequence 50 AA;

Query Match      100.0%; Score 69; DB 4; Length 50;
Best Local Similarity 10.8%; Pred. No. 1e+03;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db  11 CIRCCGSHVQSHSLTHSRNSIRIGRLIRSECLEC 47

RESULT 13
ABG47636
ID  ABG47636 standard; peptide; 50 AA.
XX
AC  ABG47636;
XX
DT  25-FEB-2003 (first entry)
XX
DE  Human liver peptide, SEQ ID No 26284.
XX
KW  Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX  hypercholesterolaemia; coronary heart disease.
XX
OS  Homo sapiens.
XX
PN  WO200157273-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US000664.
XX
PR  04-FEB-2000; 2000US-0180312P.
XX  26-MAY-2000; 2000US-0207456P.
XX  30-JUN-2000; 2000US-00608408.
XX  03-AUG-2000; 2000US-00632366.
XX  21-SEP-2000; 2000US-0234687P.
XX  27-SEP-2000; 2000US-0236359P.
XX  04-OCT-2000; 2000GB-00024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR  WPI; 2001-483446/52.
XX
PT  Single exon nucleic acid probes for analyzing gene expression in human
XX  brains.
XX
PS  Example 4; SEQ ID NO 25696; 650pp + Sequence Listing; English.
XX
CC  The present invention provides a number of single exon nucleic acid
XX  probes which are derived from genomic sequences expressed in the human
XX  brain. They can be used to measure gene expression in brain cell samples,
XX  which may enable the diagnosis and improved treatment of nervous system
XX  diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX  epilepsy and cancers. The present sequence is a protein encoded by one of
XX  the probes of the invention
XX
SQ  Sequence 50 AA;
```

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488898/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 PT
 XX Claim 27; SEQ ID NO 26284; 658pp; English.
 XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 50 AA;
 SQ
 Query Match 100.0%; Score 69; DB 4; Length 50;
 Best Local Similarity 10.8%; Pred. No. 1e+03;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
 DB 11 CIRCSCGVHVSRLTHSRNIRIGRLIRSECLC 47
 RESULT 14
 AA001583
 ID AA001583 standard; protein; 50 AA.
 AC AA001583;
 DT 09-OCT-2001 (first entry)
 XX Peptide #265 encoded by probe for measuring human breast gene expression.
 DE Probe; human; breast disease; breast cancer; development disorder;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 KW
 OS Homo sapiens.
 XX
 XX WO200157270-A2.
 PN
 XX
 XX 09-AUG-2001.
 PD
 XX
 XX 29-JAN-2001; 2001WO-US000661.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-476286/51.
 DR
 XX Novel single exon nucleic acid probe used to measuring gene expression in
 PT a human breast.
 PT
 XX

PS Claim 27; SEQ ID NO 10323; 322pp; English.
 XX The present invention relates to novel single exon nucleic acid probes
 CC (see AA100010-AA110067). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for measuring human gene expression in
 CC a human breast sample, where the probe hybridises at high stringency to a
 CC nucleic acid expressed in the human breast. The probes are useful for
 CC predicting, diagnosing, grading, staging, monitoring and prognosing
 CC diseases of the human breast, particularly those diseases with polygenic
 CC aetiology. The diseases include: breast cancer, disorders of development,
 CC inflammatory diseases of the breast, fibrocystic changes, proliferative,
 CC breast disease and non-carcinoma tumours. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 50 AA;
 SQ
 Query Match 100.0%; Score 69; DB 4; Length 50;
 Best Local Similarity 10.8%; Pred. No. 1e+03;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
 DB 11 CIRCSCGVHVSRLTHSRNIRIGRLIRSECLC 47
 RESULT 15
 ABG35618
 ID ABG35618 standard; peptide; 50 AA.
 AC ABG35618;
 XX
 XX 19-AUG-2002 (first entry)
 DT
 XX Human peptide encoded by genome-derived single exon probe SEQ ID 25283.
 DE Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200186003-A2.
 PN
 XX
 XX 15-NOV-2001.
 PD
 XX
 XX 30-JAN-2001; 2001WO-US000665.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2002-114183/15.
 DR
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 PT
 XX Claim 27; SEQ ID NO 25283; 634pp; English.
 PS

1	69	100.0	37	4	US-09-489-847-294	Sequence 294, App
2	69	100.0	39	1	US-08-036-555B-40	Sequence 40, Appl
3	69	100.0	39	1	US-08-469-569-40	Sequence 40, Appl
4	69	100.0	39	1	US-08-249-322A-40	Sequence 40, Appl
5	69	100.0	39	1	US-08-469-526A-40	Sequence 40, Appl
6	69	100.0	39	2	US-08-734-591A-40	Sequence 40, Appl
7	69	100.0	39	2	US-08-469-660-40	Sequence 40, Appl
8	69	100.0	39	3	US-08-735-021-40	Sequence 40, Appl
9	69	100.0	39	3	US-08-734-664A-40	Sequence 40, Appl
10	69	100.0	39	5	PCT-US94-05083C-40	Sequence 40, Appl
11	69	100.0	39	5	PCT-US95-06846A-40	Sequence 40, Appl
12	69	100.0	43	3	US-09-230-196-19	Sequence 19, Appl
13	69	100.0	45	3	US-08-900-230-46	Sequence 46, Appl
14	69	100.0	46	2	US-08-691-814B-38	Sequence 38, Appl
15	69	100.0	47	2	US-08-691-814B-39	Sequence 39, Appl
16	69	100.0	47	3	US-08-482-085B-91	Sequence 91, Appl
17	69	100.0	50	3	US-08-900-230-8	Sequence 8, Appl
18	69	100.0	50	4	US-09-270-767-34381	Sequence 34381, A
19	69	100.0	50	4	US-09-270-767-49598	Sequence 49598, A
20	69	100.0	54	3	US-08-851-843A-183	Sequence 183, App
21	69	100.0	54	3	US-08-974-549A-302	Sequence 302, App
22	69	100.0	54	3	US-08-854-050-183	Sequence 183, App
23	69	100.0	54	3	US-09-430-323-183	Sequence 183, App
24	69	100.0	54	4	US-09-402-181B-302	Sequence 302, App
25	69	100.0	54	4	US-09-721-456-302	Sequence 302, App
26	69	100.0	54	6	5258287-15	Patent No. 5258287
27	69	100.0	54	6	5258287-15	Patent No. 5258287

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RESULT 3
US-08-469-569-40
; Sequence 40, Application US/08469569
; Patent No. 5606032
; GENERAL INFORMATION:
; APPLICANT: Goodheartl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

```

```

RESULT 4
US-08-249-322A-40
; Sequence 40, Application US/08249322A
; Patent No. 5716930
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

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; APPLICATION NUMBER: 08/470,335
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-734-591A-40

Query Match 100.0%; Score 69; DB 2; Length 39;
Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
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Db 3 CGCKCCTTTCACRACAGAGTCTCTCTCTCAGC 39

RESULT 7
US-08-469-660-40
; Sequence 40, Application US/08469660
; Patent No. 5876973
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 0211-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,660
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,396
; FILING DATE: 29-JAN-1993

; APPLICATION NUMBER: 07/984,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-469-660-40

Query Match 100.0%; Score 69; DB 2; Length 39;
Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
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Db 3 CGCKCCTTTCACRACAGAGTCTCTCTCTCAGC 39

RESULT 8
US-08-735-021-40
; Sequence 40, Application US/08735021B
; Patent No. 6194377
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROEBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/00200L
; CURRENT APPLICATION NUMBER: US/08/735,021B
; CURRENT FILING DATE: 1996-10-22
; EARLIER APPLICATION NUMBER: 08/472,065
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/965,173
; EARLIER FILING DATE: 1992-10-23
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Bos taurus
; US-08-735-021-40

Query Match 100.0%; Score 69; DB 3; Length 39;
Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXCX 37
|::||:||||:||||:||||:||||:||||:|:|
Db 3 GCCKCCRTTACACAGAGGTCTTCCTTCTCAGC 39

RESULT 9
US-08-734-664A-40
; Sequence 40, Application US/08734664A
; Patent No. 6204241
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,664A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,322
; FILING DATE: 26-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-734-664A-40

```

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Query Match      100.0%; Score 69; DB 3; Length 39;
Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels

Qy      1 CXKXXXXXXXCCCCCCCCCCCCCCCCCCCCCCCCXCC 37
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Db      3 GCCKCCRTTACRCAGAGGCTTCTCTCTTCAGC 39

RESULT 10
PCT-US94-05083C-40
; Sequence 40, Application PC/TUS9405083C
; GENERAL INFORMATION:
; APPLICANT: Robert Sklar, Mark Marchionni,
; APPLICANT: David I. Gwynne
; TITLE OF INVENTION: METHODS FOR ALTERING
; TITLE OF INVENTION: MUSCLE CONDITION
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360
; MEDIUM TYPE: kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05083C
; FILING DATE: 06-MAY-94
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,204
; FILING DATE: 08-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059,022
; FILING DATE: 06-May-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/028W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US94-05083C-40

Query Match      100.0%; Score 69; DB 5; Length 39;
Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels

Qy      1 CXKXXXXXXXCCCCCCCCCCCCCCCCCCCCCCCCXCC 37
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Db      3 GCCKCCRTTACRCAGAGGCTTCTCTCTTCAGC 39

RESULT 11
PCT-US95-06846A-40
; Sequence 40, Application PC/TUS9506846A
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew David; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchio
; APPLICANT: Chen, Maio Su; Hiles, Ian

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Query Match          100.0%; Score 69; DB 3; Length 39;
Best Local Similarity 10.8%; Pred. NO. 1.1e-02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
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Db 3 CGCKCRRITCARGAAGGTCCTCTCTCAGC 39

RESULT 10
PCT-US94-05083C-40
; Sequence 40, Application PC/TUS9405083C
; GENERAL INFORMATION:
; APPLICANT: Robert Sklar, Mark Marchionni,
; APPLICANT: David I. Gwynne
; TITLE OF INVENTION: METHODS FOR ALTERING
; TITLE OF INVENTION: MUSCLE CONDITION
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360
; MEDIUM TYPE: kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05083C
; FILING DATE: 06-MAY-94
; CLASSIFICATION:
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; FILING DATE: 08-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059,022
; FILING DATE: 06-MAY-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/028W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US94-05083C-40

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Best Local Similarity 10.8%; Pred. NO. 1.1e-02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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Db 3 CGCKCRRITCARGAAGGTCCTCTCTCAGC 39

RESULT 11
PCT-US95-06846A-40
; Sequence 40, Application PC/TUS9506846A
; GENERAL INFORMATION:
; APPLICANT: Goodale, Andrew David; Stroobant, Paul;
; APPLICANT: Luigia; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;

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; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06846A
; FILING DATE: 25-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,322
; FILING DATE: 26-MAY-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5250.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US95-06846A-40

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Query Match 100.0%; Score 69; DB 5; Length 39;
Best Local Similarity 10.8%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 CGCCKCCTTACACAGAGTCTTCTCTTCTCAGC 39

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RESULT 12
US-09-230-196-19
; Sequence 19, Application US/09230196
; Patent No. 6307035
; GENERAL INFORMATION:
; APPLICANT: Rauscher III, Frank J.
; APPLICANT: Jensen, David E.
; TITLE OF INVENTION: BRCA1 Associated Protein (BAP-1) and
; TITLE OF INVENTION: Uses Therefor

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; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/230,196
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,997
; FILING DATE: 02-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/038,109
; FILING DATE: 19-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST68BUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-230-196-19

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Query Match 100.0%; Score 69; DB 3; Length 43;
Best Local Similarity 10.8%; Pred. No. 1.3e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
US-08-900-230-46
; Sequence 46, Application US/08900230
; Patent No. 6329197
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of The Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,230
; FILING DATE: 23-JUL-1997
; CLASSIFICATION: 435

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-763-616-2

Perfect score: 69
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Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	69	100.0	39	8	US-08-736-019-40
3	69	100.0	39	17	US-10-844-218-40
4	69	100.0	45	8	US-08-900-230-46
5	69	100.0	47	14	US-10-029-386-33022
6	69	100.0	50	8	US-08-900-230-8
7	69	100.0	50	9	US-09-864-761-33565
8	69	100.0	50	17	US-10-864-774-8
9	69	100.0	53	15	US-10-347-542-31
10	69	100.0	54	9	US-09-843-676-183
11	69	100.0	54	10	US-09-438-486-183
12	69	100.0	54	14	US-10-053-758-183
13	69	100.0	54	14	US-10-054-295-183
					Sequence 294, App
					Sequence 40, Appl
					Sequence 8, Appl
					Sequence 46, Appl
					Sequence 33022, A
					Sequence 8, Appl
					Sequence 33565, A
					Sequence 31, Appl
					Sequence 183, App
					Sequence 183, App
					Sequence 183, App

14	69	100.0	54	14	US-10-054-611-183	Sequence 183, App
15	69	100.0	54	14	US-10-029-386-33820	Sequence 33820, A
16	69	100.0	54	15	US-10-325-810-302	Sequence 302, App
17	69	100.0	54	17	US-10-877-146-302	Sequence 302, App
18	69	100.0	55	13	US-10-125-062-4	Sequence 4, Appl
19	69	100.0	55	17	US-10-900-857-4	Sequence 4, Appl
20	69	100.0	57	15	US-10-424-599-198399	Sequence 198399, A
21	69	100.0	60	9	US-09-864-761-35391	Sequence 35391, A
22	69	100.0	60	15	US-10-424-599-191604	Sequence 191604, A
23	69	100.0	63	9	US-09-864-761-35525	Sequence 35525, A
24	69	100.0	66	15	US-10-424-599-159902	Sequence 159902, A
25	69	100.0	66	15	US-10-424-599-246606	Sequence 246606, A
26	69	100.0	66	17	US-10-926-683-941	Sequence 941, App
27	69	100.0	67	15	US-10-424-599-188842	Sequence 188842, A
28	69	100.0	68	15	US-10-424-599-195690	Sequence 195690, A
29	69	100.0	68	15	US-10-424-599-245913	Sequence 245913, A
30	69	100.0	68	16	US-10-437-963-129827	Sequence 129827, A
31	69	100.0	69	15	US-10-424-599-251423	Sequence 251423, A
32	69	100.0	70	15	US-10-347-542-32	Sequence 32, Appl
33	69	100.0	70	15	US-10-424-599-202673	Sequence 202673, A
34	69	100.0	71	9	US-09-864-761-42524	Sequence 42524, A
35	69	100.0	71	14	US-10-011-931-14	Sequence 14, Appl
36	69	100.0	71	14	US-10-011-931-15	Sequence 15, Appl
37	69	100.0	71	14	US-10-011-931-30	Sequence 30, Appl
38	69	100.0	71	14	US-10-011-931-31	Sequence 31, Appl
39	69	100.0	71	14	US-10-011-931-32	Sequence 32, Appl
40	69	100.0	71	14	US-10-011-931-33	Sequence 33, Appl
41	69	100.0	71	14	US-10-269-806-114	Sequence 114, App
42	69	100.0	71	16	US-10-767-701-33777	Sequence 33777, A
43	69	100.0	71	17	US-10-985-299-14	Sequence 14, Appl
44	69	100.0	71	17	US-10-985-299-15	Sequence 15, Appl
45	69	100.0	71	17	US-10-985-299-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-351-334-294
; Sequence 294, Application US/10351334
; Publication No. US20040034196A1
; GENERAL INFORMATION:
; APPLICANT: Komatseoulis et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P2
; CURRENT APPLICATION NUMBER: US/10/351,334
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/350,898
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/489,847
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: PCT/US99/17130
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 60/095,486
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/096,319
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: 60/095,454
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 60/095,455
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 294
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-351-334-294

Query Match 100.0%; Score 69; DB 15; Length 37;
Best Local Similarity 10.8%; Pred. No. 5.8e+02;

Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

US-08-736-019-40

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Best Local Similarity 100.0%; Score 69; DB 8; Length 39;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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US-08-736-019-40

Sequence 40, Application US/08736019
Publication No. US2003020779A1
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew
APPLICANT: Stroobant, Paul
APPLICANT: Minghetti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Marchionni, Mark
APPLICANT: Chen, Mario
APPLICANT: Hiles, Ian
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible Pentium
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/736,019
FILING DATE: 22-OCT-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,833
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 91 07566.3
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200Q
TELEPHONE: (617) 428-0200
TELEFAX: (617) 428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 39
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear

QY 1 CXCXCCCCCCCCCCCCCCCCCCCCCCCCCCXC 37
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US-08-736-019-40

Sequence 40, Application US/10844218
Publication No. US2005010666A1
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew; Stroobant, Paul; Minghetti, Luisa; Su, Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/844,218
FILING DATE: 12-AUG-2004
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tsai, Christine H., 266
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LJD 5250.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 39
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
TELECOMMUNICATION INFORMATION:
SEQ ID NO: 40:
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-844-218-40

Query Match
Best Local Similarity 100.0%; Score 69; DB 17; Length 39;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CXCXCCCCCCCCCCCCCCCCCCCCCCCCCCXC 37


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; Sequence 33565, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33565
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000091.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 11
; OTHER INFORMATION: EST HUMAN HIT: A1890146.1, EVALUAE 3.40e+00
; OTHER INFORMATION: SWISSPROT HIT: Q61282, EVALUAE 6.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AA932293.1, EVALUAE 5.10e+00
; US-09-864-761-33565
; Query Match 100.0%; Score 69; DB 9; Length 50;
; Best Local Similarity 10.8%; Pred. No. 8.6e+02;
; Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
DB 11 CIRCCGVHVQSHSLTHSRNSIRIGRLIRSECLC 47
RESULT 8
US-10-864-774-8
; Sequence 8, Application US/10864774
; Publication No. US20050090646A1
; GENERAL INFORMATION:
; APPLICANT: SULLIVAN, SEAN M.
; TITLE OF INVENTION: GENE DELIVERY TO TUMORS
; FILE REFERENCE: 5853-337-1W0
; CURRENT APPLICATION NUMBER: US/10/864,774
; CURRENT FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-864-774-8
; Query Match 100.0%; Score 69; DB 17; Length 50;
; Best Local Similarity 10.8%; Pred. No. 8.6e+02;
; Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
DB 9 CTTCACTATTTTCATTCCTCAATGGGTGACTTTGCTTC 45
RESULT 9
US-10-347-542-31
; Sequence 31, Application US/10347542
; Publication No. US20040009530A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David
; APPLICANT: No. US20040009530alk, Steffen
; APPLICANT: Wagstrom, Christopher
; APPLICANT: Wu, Jiangchun
; APPLICANT: Uemura, Robyn
; TITLE OF INVENTION: ENGINEERED BINDING PROTEINS
; FILE REFERENCE: 11001-006-999
; CURRENT APPLICATION NUMBER: US/10/347,542
; CURRENT FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
; US-10-347-542-31
; Query Match 100.0%; Score 69; DB 15; Length 53;
; Best Local Similarity 10.8%; Pred. No. 9.3e+02;
; Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
DB 5 CKICGYIDBDAGDPDNGISGPKFELPDDWVCPIC 41
RESULT 10
US-09-843-676-183
; Sequence 183, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru

```

Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 183:
US-09-843-676-183
Query Match 100.0%; Score 69; DB 9; Length 54;
Best Local Similarity 10.8%; Pred. No. 9.5e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
Db 3 CSACSTTSGRGAPASWAPLCWMTISTGPGAPSCVC 39
RESULT 11
US-09-438-486-183
Sequence 183, Application US/09/438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1el Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-438-486-183
Query Match 100.0%; Score 69; DB 10; Length 54;
Best Local Similarity 10.8%; Pred. No. 9.5e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXC 37
Db 3 CSACSTTSGRGAPASWAPLCWMTISTGPGAPSCVC 39
RESULT 12
US-10-053-758-183
Sequence 183, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco

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;
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053.758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US/08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US/08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/724,643
; FILING DATE: 01-OCT-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 183:
US-10-053-758-183

Query Match 100.0%; Score 69; DB 14; Length 54;
Best Local Similarity 10.8%; Pred. No. 9.5e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 3 CSACSTTSGRGAPASWAPLCWAWTISTGPGAPSCVC 39

RESULT 13
US-10-054-295-183
; Sequence 183, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US/08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/724,643
; FILING DATE: 01-OCT-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 183:
US-10-054-295-183

Query Match 100.0%; Score 69; DB 14; Length 54;
Best Local Similarity 10.8%; Pred. No. 9.5e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 3 CSACSTTSGRGAPASWAPLCWAWTISTGPGAPSCVC 39

RESULT 14
US-10-054-611-183
; Sequence 183, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
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;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;;   NAME: Apple, Randolph T.
;;   REGISTRATION NUMBER: 36,429
;;   REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;;   TELEPHONE: (415) 576-0200
;;   TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 183:
;;   SEQUENCE CHARACTERISTICS:
;;     LENGTH: 54 amino acids
;;     TYPE: amino acid
;;     STRANDEDNESS: <Unknown>
;;     TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 183:
US-10-054-611-183
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Query Match      100.0%; Score 69; DB 14; Length 54;
Best Local Similarity 10.8%; Pred. No. 9.5e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 37
Db 3 CSACSTSGRGAPASWAPLCWMTSTGPGAPSCVC 39
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RESULT 15

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US-10-029-386-33820
; Sequence 33820, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: EXPRESSION ANALYSIS TWO
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33820
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002455.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: SWISSPROT HIT: P34088, EVALUATION 1.60e+00
US-10-029-386-33820
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Query Match      100.0%; Score 69; DB 14; Length 54;
Best Local Similarity 10.8%; Pred. No. 9.5e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 37
Db 3 CPOCWAQSGHRCMCNTVWPRHSVWLWLVTPICRC 39
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Search completed: May 27, 2005, 00:48:47
Job time : 149 secs

§ PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2005, 00:26:25 ; Search time 39 Seconds
(without alignments)
91.283 Million cell updates/sec

Title: US-09-763-616-2
Perfect score: 69
Sequence: 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXC 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:**

2: PIR1:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	52	1 A33173	rubredoxin [valida
2	69	100.0	52	1 JX0241	rubredoxin - Desul
3	69	100.0	52	1 RUDV	rubredoxin [valida
4	69	100.0	52	1 RUDVEG	rubredoxin [valida
5	69	100.0	52	2 S65620	rubredoxin - Helio
6	69	100.0	52	2 G71256	probable rubredoxi
7	69	100.0	53	1 A27537	rubredoxin - Chlor
8	69	100.0	53	1 A33182	rubredoxin - Clost
9	69	100.0	53	1 JU0127	rubredoxin - "Buty
10	69	100.0	53	2 H69359	rubredoxin (rd-1)
11	69	100.0	53	2 H72348	rubredoxin - Therm
12	69	100.0	53	2 B69075	rubredoxin - Metha
13	69	100.0	53	2 E75136	rubredoxin PAB7224
14	69	100.0	54	1 JU0074	rubredoxin - Clost
15	69	100.0	54	1 RUCLEP	rubredoxin [valida
16	69	100.0	54	1 RUCLEP	rubredoxin [valida
17	69	100.0	54	2 G97241	rubredoxin [import
18	69	100.0	54	2 I39520	rubredoxin - Acine
19	69	100.0	54	2 AE2375	rubredoxin [import
20	69	100.0	55	2 E70593	probable rubA prot
21	69	100.0	55	2 H82976	rubredoxin PAS350
22	69	100.0	55	2 A82977	rubredoxin PAS351
23	69	100.0	55	2 S25774	testis-specific pr
24	69	100.0	56	1 WTFE	testis-specific pr
25	69	100.0	56	2 H81133	rubredoxin NMB0993
26	69	100.0	56	2 F69517	rubredoxin (fdx-8)
27	69	100.0	57	2 B82814	rubredoxin XF0379
28	69	100.0	57	2 B97333	rubredoxin [import
29	69	100.0	58	2 B42960	ferredoxin 2[4Fe-4

ALIGNMENTS

RESULT 1

A33173

rubredoxin [validated] - Clostridium thermosaccharolyticum

C;Species: Clostridium thermosaccharolyticum, Clostridium tartarivorum

C;Date: 30-Apr-1991 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

C;Accession: A33173

R;Meyer, J.; Gagnon, J.; Sieker, L.C.; Van Dorsselaer, A.; Moulis, J.M.

Biochem. J. 271, 839-841, 1990

A;Title: Rubredoxin from Clostridium thermosaccharolyticum. Amino acid sequence, mass-

A;Reference number: A33173; MUID:91058526; PMID:2244884

A;Accession: A33173

A;Molecule type: protein

A;Residues: 1-52 <MEY>

A;Cross-references: UNIPROT:P19500

C;Superfamily: rubredoxin; rubredoxin homology

C;Keywords: electron transfer; iron; metalloprotein

F;3-49/Domain: rubredoxin homology <RUB>

F;1/Modified site: N-formylmethionine #status experimental

F;6,9,39,42/Binding site: iron (Cys) #status predicted

Query Match 100.0%; Score 69; DB 1; Length 52;
Best Local Similarity 10.8%; Pred. No. 3.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXC 37

Db 6 CTVCGYIDPEVGDPTQNIPTGKFDLDDWVCPDC 42

RESULT 2

JX0241

rubredoxin - Desulfovibrio vulgaris (strain Miyazaki)

C;Species: Desulfovibrio vulgaris

C;Date: 10-Jun-1993 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004

C;Accession: JX0241

R;Shimizu, F.; Ogata, M.; Yagi, T.; Wakabayashi, S.; Mateubara, H.

Biochimie 71, 1171-1177, 1989

A;Title: Amino acid sequence and function of rubredoxin from Desulfovibrio vulgaris Miy

A;Reference number: JX0241; MUID:90234754; PMID:2561345

A;Accession: JX0241

A;Molecule type: protein

A;Residues: 1-52 <SHI>

A;Cross-references: UNIPROT:P15412

C;Superfamily: rubredoxin; rubredoxin homology

C;Keywords: electron transfer; iron; metalloprotein

F;3-49/Domain: rubredoxin homology <RUB>

F;1/Modified site: N-formylmethionine (partial) #status experimental

F;6,9,39,42/Binding site: iron (Cys) #status predicted

Query Match 100.0%; Score 69; DB 1; Length 52;
Best Local Similarity 10.8%; Pred. No. 3.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

submitted to the Brookhaven Protein Data Bank, March 1988

A;Reference number: A50332; PDB:1RDXG
A;Contents: annotation; X-ray crystallography, 1.4 angstroms, residues 1-52
R;Frey, M.; Sieker, L.; Payan, E.; Haser, R.; Bruschi, M.; Pepe, G.; Le Gall, J.
J. Mol. Biol. 197, 525-541, 1987
A;Title: Rubredoxin from Desulfococcus gigas. A molecular model of the oxidized form at
A;Reference number: A46624; PMID:88155649; PMID:3441010
A;Contents: annotation; X-ray crystallography, 1.4 angstroms
C;Superfamily: rubredoxin; rubredoxin homology
C;Keywords: blocked amino end; electron transfer; iron; metalloprotein
F;3-49/Domain: rubredoxin homology <SUB>
F;1/Modified site: N-formylmethionine #status experimental
F;6,9,39,42/Binding site: Iron (Cys) #status experimental

Query Match 100.0%; Score 69; DB 1; Length 52;
Best Local Similarity 10.8%; Pred. No. 3.le+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXKXXXXXXXXXXXXXXXKKXKXXXXXXXXXXXXCKXC 37
 |::|::::::::::||:::::::::::::||:
Db 6 CTVCVGYDPAKGDPDGSGIKPGTKFDLPDDWACPVC 42

RESULT 5
S65620
rubredoxin - Helicobacillus mobilis
C;Species: Helicobacillus mobilis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65620
R;Lee, W.Y.; Brune, D.C.; LoBrutto, R.; Blankenship, R.E.
Arch. Biochem. Biophys. 318, 80-88, 1995
A;Title: Isolation, characterization, and primary structure of rubredoxin from the phot
A;Reference number: S65620; PMID:95243660; PMID:7726577
A;Accession: S65620
A:Molecule type: protein
A;Residues: 1-52 <LEE>
A;Cross-references: UNIPROT:P56263
C;Comment: Rubredoxin is a non-heme iron protein and substitutes for ferredoxin in some
C;Superfamily: rubredoxin; rubredoxin homology
C;Keywords: electron transfer; hydrocarbon hydroxylation; iron; metalloprotein
F;3-49/Domain: rubredoxin homology <SUB>
F;1/Modified site: N-formylmethionine #status experimental
F;6,9,39,42/Binding site: Iron (Cys) #status predicted

Query Match 100.0%; Score 69; DB 2; Length 52;
Best Local Similarity 10.8%; Pred. No. 3.le+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXKXXXXXXXXXXXXXXXKKXKXXXXXXXXXXXXCKXC 37
 |::|::::::::::||:::::::::::::||:
Db 6 CLVCGVVYPADKPDPDHGIAPGTAFEDPADWCPLC 42

RESULT 6
G71256
probable rubredoxin - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: G71256
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gar
rison, J.; Khaliq, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; PMID:98332770; PMID:9665876
A;Accession: G71256
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-52 <COL>
A;Cross-references: UNIPROT:O83956; GB:AEO01266; GB:AEO00520; NID:g3323309; PIDN:AAC65!
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0991

JU0127
 rubredoxin - "Butyribacterium methylotrophicum"
 C:Species: "Butyribacterium methylotrophicum"
 C:Date: 31-Mar-1990 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
 C:Accession: JU0127
 R:Saeki, K.; Yao, Y.; Wakabayashi, S.; Shen, G.J.; Zeikus, J.G.; Matsubara, H.
 J. Biochem. 106, 658-662, 1989
 A:Title: Ferredoxin and rubredoxin from Butyribacterium methylotrophicum: complete prim
 A:Reference number: A91913; MUID:90110065; PMID:2606914
 A:Accession: JU0127
 A:Molecule type: protein
 A:Residues: 1-53 <SAE>
 A:Cross-references: UNIPROT:P14071
 C:Comment: Rubredoxin is a nonheme iron protein and substitutes for ferredoxin in some
 C:Superfamily: rubredoxin; rubredoxin homology
 C:Keywords: electron transfer; iron; metalloprotein
 F:3-49/Domain: rubredoxin homology <RUB>
 F:6,9,39,42/Binding site: iron (Cys) #status predicted

Query Match 100.0%; Score 69; DB 1; Length 53;
 Best Local Similarity 10.8%; Pred.No. 3.1e+02;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
 [...]::::::::::::::::::::::::::|:
 DB 6 CDICGVYDPAVGDPNGVAPGTAFADLPEDWVCPEC 42

RESULT 10
 H69359
 rubredoxin (rd-1) homolog - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: H69359
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: H69359
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-53 <KLE>
 A:Cross-references: UNIPROT:O29381; GB:AE001043; GB:AE000782; NID:g2689366; PIDN:AA8903
 C:Superfamily: rubredoxin; rubredoxin homology
 C:Keywords: iron; metalloprotein
 F:3-49/Domain: rubredoxin homology <RUB>
 F:6,9,39,42/Binding site: iron (Cys) #status predicted

Query Match 100.0%; Score 69; DB 2; Length 53;
 Best Local Similarity 10.8%; Pred.No. 3.1e+02;
 Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
 [...]::::::::::::::::::::::::::|:
 DB 6 CTICGVYDPAVGDPNGVAPGTAFADLPEDWVCPEC 42

RESULT 11
 H72348
 rubredoxin - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: H72348
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D. D.
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se-
 A:Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: H72348
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-53 <ARN>
A;Cross-references: UNIPROT.Q9WZC7; GB:AEO01739; GB:AEO00512; NID:g4981176; PIDN:AAD3574
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0659
C;Superfamily: rubredoxin; rubredoxin homology
C;Keywords: iron; metalloprotein
F;3-49/Domain: rubredoxin homology <RUB>
F;6,9,39,42/Binding site: Iron (Cys) #status predicted

Query Match 100.0%; Score 69; DB 2; Length 53;
Best Local Similarity 10.8%; Pred. No. 3.le+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXKXXXXXXX XXXXXXXXXXXXXXXXXXXX CXCX 37
 |:|:::||||||:||||||:|
Db 6 CKLCGYIDPEQGDPDSGIEPGTFEDLPDDWCPLC 42

RESULT 12

B69075
rubredoxin - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: B69075
F;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A>Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional reference number A69000; PMID:9371463
A;Reference numbers: A69000; PMID:9371463
A;Accession: B69075
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: RNA
A;Residues: 1-53 <MTH>
A;Cross-references: UNIPROT.O26259; GB:AEO00804; GB:AEO00666; NID:g2621196; PIDN:AAB8466
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH156
C;Superfamily: rubredoxin; rubredoxin homology
C;Keywords: iron; metalloprotein
F;3-49/Domain: rubredoxin homology <RUB>
F;6,9,39,42/Binding site: iron (Cys) #status predicted

Query Match 100.0%; Score 69; DB 2; Length 53;
Best Local Similarity 10.8%; Pred. No. 3.le+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXKXXXXXXX XXXXXXXXXXXXXXXXXXXX CXCX 37
 |:|:::||||||:||||||:|
Db 6 CQMCGYIDPEEGPVSIGAGTFFDLPDDWCPCV 42

RESULT 13

E75136
rubredoxin BAB7224 [similarity] - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: E75136
R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Reference number: A75001
A;Accession: E75136
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-53 <RAW>
A;Cross-references: UNIPROT.Q9W099; GB:AJ24285; GB:AL096836; NID:g5458067; PIDN:CAB4980
A;Experimental source: strain Orsay
C;Genetics:

Search completed: May 27, 2005, 00:36:06
Job time : 40 secs

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
DR EMBL; AE011987; AAM38257.1; -
DR HSSP; P00268; IIRO.
DR GO; GO:0046872; F-metal ion binding; IEA.
DR GO; GO:0006118; P-electron transport; IEA.
DR InterPro; IPR001052; Rubredoxin.
DR ProDom; PD001610; Rubredoxin; 1.
DR PROSITE; PS00202; RUBREDOXIN; UNKNOWN 1.
DR PROSITE; PS0903; RUBREDOXIN_LIKE; 1.
DR Complete proteome.
KW SEQUENCE 51 AA; 5706 MW; 6E26E27D93530E8F CRC64;
SQ SEQUENCE 51 AA; 5706 MW; 6E26E27D93530E8F CRC64;

Query Match 100.0%; Score 69; DB 2; Length 51;
Best Local Similarity 10.8%; Pred. No. 5.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 2 CVVCGFLYHEADGIPBEGIAPGTWQVDPDWTCPDC 38

RESULT 4
RUB2 CHLTE
ID RUB2 CHLTE STANDARD; PRT; 52 AA.
AC P58993;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Rubredoxin 2 (Rd 2).
GN Namesrub2; Synonyms=rbr-2; OrderedLocusNames=CTII101;
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobaculum.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parksey D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
CC -!- FUNCTION: Serves as an electron acceptor for pyruvate ferredoxin
CC oxidoreductase (PFOR) (By similarity).
CC -!- COPACTOR: Binds 1 iron(III) ion per subunit (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the rubredoxin family.
CC -!- SIMILARITY: Contains 1 rubredoxin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; AE012873; AAM72334.1; -
DR HSSP; P24297; 1BQ8.
DR TIGR; CTII01; -.
DR InterPro; IPR004039; Rubredox.

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Query Match 100.0%; Score 69; DB 1; Length 52;
Best Local Similarity 10.8%; Pred. No. 5.2e+02;
Matches 4; Conservative 33; Mismatches 0; Indels

Db 6 CTVGGEYDPAEGDPNGVKGPTGFDLPAWVCPVC 42

RESULT 8

RUBR_DESVM STANDARD; PRT; 52 AA.
AC P15412;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Rubredoxin (Rd).
GN Name-rub;
OS Desulfovibrio vulgaris (strain Miyazaki).
OC Bacteria; Proteobacteria; Deitaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=883;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate F;
RX MEDLINE=97236449; PubMed=9116039; DOI=10.1016/S0167-4781(96)00203-5;
RA Kitamura M., Koshino Y., Kamikawa Y., Kohno K., Kojima S., Miura K.,
RA Sagata T., Akuteau H., Kumagai I., Nakaya T.;
RT "Cloning and expression of the rubredoxin gene from Desulfovibrio
RT vulgaris (Miyazaki F) -- comparison of the primary structure of
RT desulfoferredoxin.";
RL Biochim. Biophys. Acta 1351:239-247(1997).
RN [2]
RP SEQUENCE.
RX MEDLINE=90234754; PubMed=2561345; DOI=10.1016/0300-9084(89)90020-5;
RA Shimizu F., Ogata M., Yagi T., Wakabayashi S., Matsubara H.;
RT "Amino acid sequence and function of rubredoxin from Desulfovibrio
RT vulgaris Miyazaki.";
RL Biochimie 71:1171-1177(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RC STRAIN=IAM 12604;
RX MEDLINE=99190893; PubMed=10089348; DOI=10.1107/S0907444998011810;
RA Misaki S., Morimoto Y., Ogata M., Yagi T., Higuchi Y., Yasuoka N.;
RT "Structure determination of rubredoxin from Desulfovibrio vulgaris
RT Miyazaki F in two crystal forms";
RL Acta Crystallogr. D 55:408-413(1999).
CC -1- FUNCTION: Rubredoxin is a small nonheme, iron protein lacking
CC acid-labile sulfide. Its single Fe, chelated to 4 Cys, functions
CC as an electron acceptor and may also stabilize the conformation of
CC the molecule.
CC -1- FUNCTION: Electron acceptor for cytoplasmic lactate dehydrogenase.
CC -1- COFACTOR: Binds 1 iron(III) ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the rubredoxin family.
CC -1- SIMILARITY: Contains 1 rubredoxin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D76419; BAA1175.1; -;
DR PIR; JX0241.
DR PDB; 1RDV; X-ray; @=1-52.
DR PDB; 2RDV; X-ray; A/B/C=1-52.
DR InterPro; IPR004039; Rubredox.
DR InterPro; IPR001052; Rubredoxin.
DR Pfam; PF00301; Rubredoxin; 1.
DR PRINTS; PR00163; RUBREDOXIN.
DR ProDom; PD001610; Rubredox; 1.
DR PROSITE; PS00202; RUBREDOXIN; 1.
DR PROSITE; PS00903; RUBREDOXIN LIKE; 1.
KW 3D-structure; Direct protein sequencing; Electron transport;

KW Formylation; Iron; Metal-binding; Rubredoxin.
MOD RES 1 1 N-formylmethionine.
FT DOMAIN 1 52 Rubredoxin-like.
FT METAL 6 6 Iron.
FT METAL 9 9 Iron.
FT METAL 39 39 Iron.
FT METAL 42 42 Iron.
FT STRAND 4 6
FT TURN 7 9
FT STRAND 12 13
FT TURN 15 17
FT STRAND 19 19
FT TURN 20 22
FT STRAND 23 23
FT TURN 24 24
FT STRAND 26 27
FT TURN 30 32
FT HELIX 35 36
FT TURN 38 38
FT STRAND 40 42
FT TURN 45 45
FT STRAND 46 48
FT HELIX 49 52
FT STRAND 52 52
SQ SEQUENCE 52 AA; 5598 MW; 6443741ABA8063A2 CRC64;
Query Match 100.0%; Score 69; DB 1; Length 52;
Best Local Similarity 10.8%; Pred. No. 5.2e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 37
DB 6 CTVGGEYDPAEGDPNGVKGPTGFDLPAWVCPIC 42
RESULT 9
RUBR_HELMO STANDARD; PRT; 52 AA.
AC P56263;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubredoxin (Rd).
OS Helicobacillus mobilis.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;
OC Helicobacillus.
OX NCBI_TaxID=28064;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=95243660; PubMed=7726577; DOI=10.1006/abbi.1995.1207;
RA Lee W.Y., Brune D.C., Lohrutto R., Blankenship R.E.;
RT "Isolation, characterization, and primary structure of rubredoxin from
RT the photosynthetic bacterium, Helicobacillus mobilis.";
RL Arch. Biochem. Biophys. 318:80-88(1995).
CC -1- FUNCTION: Rubredoxin is a small nonheme, iron protein lacking
CC acid-labile sulfide. Its single Fe, chelated to 4 Cys, functions
CC as an electron acceptor and may also stabilize the conformation of
CC the molecule.
CC -1- COFACTOR: Binds 1 iron(III) ion per subunit (By similarity).
CC -1- MASS SPECTROMETRY: MW=5671.3; METHOD=MALDI; RANGE=1-52;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the rubredoxin family.
CC -1- SIMILARITY: Contains 1 rubredoxin-like domain.
DR PIR; S65620; S65620.
DR HSSP; P15412; 2RDV.
DR InterPro; IPR004039; Rubredox.
DR InterPro; IPR001052; Rubredoxin.
DR Pfam; PF00301; Rubredoxin; 1.
DR PRINTS; PR00163; RUBREDOXIN.
DR ProDom; PD001610; Rubredox; 1.
DR PROSITE; PS00202; RUBREDOXIN; 1.
DR PROSITE; PS00903; RUBREDOXIN LIKE; 1.
KW Direct protein sequencing; Electron transport; Formylation; Iron;
Metal-binding; Rubredoxin.

Matches	4;	Conservative	33;	Mismatches	0;	Indels	0;	Gap
Qy	i	CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37						
		: : : : : :						
Db	6	CTVCGVIYDPEKXGDPGQIGPPGTPPEELPDWVCPDC 42						
RESULT 14								
ID	Q73NVO	PRELIMINARY;	PRT;	52	AA.			
AC	Q73NVO;							
DT	05-JUL-2004	(TREMBLrel. 27, Created)						
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)						
DT	03-JUL-2004	(TREMBLrel. 27, Last annotation update)						
DE	Rubredoxin.							
GN	OrderedLocusNames=TDE1052;							
OS	Treponema denticola.							
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.							
OX	NCBI_TaxID=158;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=ATCC 35405 / DSM 14222;							
RX	PubMed=15064399; DOI=10.1073/pnas.0307639101;							
RA	Sehadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,							
RA	Dodson R.J., Davidson T.M., Deboy R.T., Fouts D.E., Haft D.H.,							
RA	Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,							
RA	Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,							
RA	Georgiev G.E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,							
RA	Shatman S., McLeod M.P., Smajic D., Howell J.K., Pal S., Amin A.,							
RA	Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,							
RA	Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;							
RT	"Comparison of the genome of the oral pathogen Treponema denticola							
RT	with other spirochete genomes.";							
RL	Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).							
CC	-1- SIMILARITY: Belongs to the rubredoxin family.							
CC	-1- SIMILARITY: Contains 1 rubredoxin-like domain.							
DR	EMBL; AS017249; AAS11541.1; -.							
DR	HSSP; P00268; 1B13.							
DR	TIGR; TDE1052; -.							
DR	GO; GO:0005489; F:electron transporter activity; IEA.							
DR	GO; GO:0046872; F:metal ion binding; IEA.							
DR	GO; GO:0006118; P:electron transport; IEA.							
DR	InterPro; IPR004039; Rubredox.							
DR	InterPro; IPR001052; Rubredoxin.							
DR	Pfam; PF00301; Rubredoxin; 1.							
DR	PRINTS; PR00163; RUBREDOXIN							
DR	ProDom; PD001610; Rubredox; 1.							
DR	PROSITE; PS00202; RUBREDOXIN; 1.							
DR	PROSITE; PS50903; RUBREDOXIN LIKE; 1.							
KW	Complete proteome; Electron transport; Iron; Metal-binding;							
KW	Rubredoxin.							
SEQ	SEQUENCE 52 AA; 5544 MW; DC1DID07223522AE CRC64;							
Query Match 100.0%; Score 69; DB 2; Length 52;								
Best Local Similarity 10.8%; Pred. No. 5.2e+02;								
Matches	4;	Conservative	33;	Mismatches	0;	Indels	0;	Gap
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Db	6	CDLCCGVVYDPAUGDPGGIAPGTAFIPDDWVCPCLC 42						
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ID	Q747S7	PRELIMINARY;	PRT;	52	AA.			
AC	Q747S7;							
DT	05-JUL-2004	(TREMBLrel. 27, Created)						
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)						
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)						
DE	Rubredoxin.							
GN	OrderedLocusNames=GSU03188;							
OS	Geobacter sulfurreducens.							
OC	Bacteria; Proteobacteria; Delta proteobacteria; Desulfuromonadales;							

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Query Match      100.0%; Score 69; DB 2; Length 52;
Best Local Similarity 10.8%; Pred. NO. 5.2e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
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Search completed: May 27, 2005, 00:35:22
Job time : 176 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2005, 00:30:06 ; Search time 495 Seconds
(without alignments)
87.306 Million cell updates/sec

Title: US-09-763-616-2

Perfect score: 69

Sequence: 1 CXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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- 25: /cgn2_6/ptodata/1/paa/US30_COMB.pcp.*
- 26: /cgn2_6/ptodata/1/paa/US31_COMB.pcp.*
- 27: /cgn2_6/ptodata/1/paa/US32_COMB.pcp.*
- 28: /cgn2_6/ptodata/1/paa/US33_COMB.pcp.*
- 29: /cgn2_6/ptodata/1/paa/US34_COMB.pcp.*
- 30: /cgn2_6/ptodata/1/paa/US35_COMB.pcp.*
- 31: /cgn2_6/ptodata/1/paa/US36_COMB.pcp.*
- 32: /cgn2_6/ptodata/1/paa/US37_COMB.pcp.*
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- 35: /cgn2_6/ptodata/1/paa/US40_COMB.pcp.*
- 36: /cgn2_6/ptodata/1/paa/US41_COMB.pcp.*
- 37: /cgn2_6/ptodata/1/paa/US42_COMB.pcp.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	69	100.0	37	1	PCT-US99-17130-287	Sequence 287, Appl
2	69	100.0	37	22	US-09-763-616-2	Sequence 294, Appl
3	69	100.0	37	29	US-10-351-334-294	Sequence 33, Appl
4	69	100.0	38	37	US-60-273-808-33	Sequence 33, Appl
5	69	100.0	38	37	US-60-278-983-33	Sequence 22, Appl
6	69	100.0	39	1	PCT-US04-15318-22	Sequence 22, Appl
7	69	100.0	39	4	US-08-011-396A-40	Sequence 40, Appl
8	69	100.0	39	6	US-08-209-204B-40	Sequence 40, Appl
9	69	100.0	39	6	US-08-209-204D-40	Sequence 40, Appl
10	69	100.0	39	6	US-08-209-204E-40	Sequence 40, Appl
11	69	100.0	39	8	US-08-461-097A-40	Sequence 40, Appl
12	69	100.0	39	8	US-08-461-097B-40	Sequence 40, Appl
13	69	100.0	39	8	US-08-466-446-40	Sequence 40, Appl
14	69	100.0	39	8	US-08-467-459A-40	Sequence 40, Appl
15	69	100.0	39	8	US-08-467-459B-40	Sequence 40, Appl
16	69	100.0	39	8	US-08-467-459C-40	Sequence 40, Appl
17	69	100.0	39	8	US-08-467-459D-40	Sequence 40, Appl
18	69	100.0	39	8	US-08-467-459E-40	Sequence 40, Appl
19	69	100.0	39	8	US-08-467-459F-40	Sequence 40, Appl
20	69	100.0	39	8	US-08-468-731A-40	Sequence 40, Appl
21	69	100.0	39	8	US-08-468-731B-40	Sequence 40, Appl
22	69	100.0	39	8	US-08-469-526A-40	Sequence 40, Appl
23	69	100.0	39	8	US-08-469-526B-40	Sequence 40, Appl
24	69	100.0	39	8	US-08-469-526C-40	Sequence 40, Appl
25	69	100.0	39	8	US-08-470-335A-40	Sequence 40, Appl
26	69	100.0	39	8	US-08-470-335B-40	Sequence 40, Appl
27	69	100.0	39	8	US-08-471-833A-40	Sequence 40, Appl
28	69	100.0	39	8	US-08-471-833B-40	Sequence 40, Appl
29	69	100.0	39	8	US-08-471-833C-40	Sequence 40, Appl
30	69	100.0	39	8	US-08-471-833D-40	Sequence 40, Appl
31	69	100.0	39	8	US-08-472-008A-40	Sequence 40, Appl
32	69	100.0	39	8	US-08-472-008B-40	Sequence 40, Appl
33	69	100.0	39	8	US-08-472-008C-40	Sequence 40, Appl
34	69	100.0	39	9	US-08-535-200A-40	Sequence 40, Appl
35	69	100.0	39	9	US-08-535-200B-40	Sequence 40, Appl
36	69	100.0	39	11	US-08-734-665A-40	Sequence 40, Appl
37	69	100.0	39	11	US-08-734-665B-40	Sequence 40, Appl
38	69	100.0	39	11	US-08-734-665C-40	Sequence 40, Appl
39	69	100.0	39	11	US-08-734-665D-40	Sequence 40, Appl
40	69	100.0	39	11	US-08-735-010A-40	Sequence 40, Appl
41	69	100.0	39	11	US-08-735-010B-40	Sequence 40, Appl
42	69	100.0	39	11	US-08-736-019A-40	Sequence 40, Appl
43	69	100.0	39	11	US-08-736-019B-40	Sequence 40, Appl
44	69	100.0	39	11	US-08-736-070A-40	Sequence 40, Appl
45	69	100.0	39	11	US-08-736-070B-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
PCT-US99-17130-287
; Sequence 287, Application PC/TUS9917130
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031.PCT
; CURRENT APPLICATION NUMBER: PCT/US99/17130
; CURRENT FILING DATE: 1999-07-29
; EARLIER FILING DATE: 1998-07-30
; EARLIER FILING DATE: 1998-07-30
; EARLIER FILING DATE: 1998-07-30
; EARLIER FILING DATE: 1998-08-05
; EARLIER FILING DATE: 1998-08-05
; EARLIER FILING DATE: 1998-08-06
; EARLIER FILING DATE: 1998-08-06
; EARLIER FILING DATE: 1998-08-06
; EARLIER FILING DATE: 1998-08-12

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; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 287
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-17130-287

Query Match      100.0%; Score 69; DB 1; Length 37;
Best Local Similarity 10.8%; Pred. No. 3.2e+03;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 1 CDDQHNTGQYQCRCKPGFYRLRRPFSAPDACKPC 37

RESULT 2
US-09-763-616-2
; Sequence 2, Application US/09763616
; GENERAL INFORMATION:
; APPLICANT: BERNARD, HANS-ULRICH
; APPLICANT: TAN, YEE JOO
; APPLICANT: BEERHEIDE, WALTER
; APPLICANT: TING, ANTHONY EUGENE
; APPLICANT: SIM, MUI MUI
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS AND METHODS
; FILE REFERENCE: BERN3001/JDB
; CURRENT APPLICATION NUMBER: US/09/763,616
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/AU99/00724
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: AU PQ1645/99
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: AU PP5733/98
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: zinc domain peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)..(3)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(33)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (35)..(36)
; OTHER INFORMATION: Variable amino acid
; OTHER INFORMATION: Variable amino acid
US-09-763-616-2

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Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
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RESULT 3
US-10-351-334-294
; Sequence 294, Application US/10351334
; GENERAL INFORMATION:
; APPLICANT: Komatsoulis et al
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; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P2
; CURRENT APPLICATION NUMBER: US/10/351,334
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/350,898
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/489,847
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: PCT/US99/17130
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 60/095,486
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/096,319
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: 60/095,454
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 60/095,455
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 294
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-351-334-294

Query Match      100.0%; Score 69; DB 29; Length 37;
Best Local Similarity 10.8%; Pred. No. 3.2e+03;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-60-273-808-33
; Sequence 33, Application US/60273808
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: D0134
; CURRENT APPLICATION NUMBER: US/60/273,808
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 38
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-273-808-33

Query Match      100.0%; Score 69; DB 37; Length 38;
Best Local Similarity 10.8%; Pred. No. 3.2e+03;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
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RESULT 5
US-60-278-983-33
; Sequence 33, Application US/60278983
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: D0134.ppt
; CURRENT APPLICATION NUMBER: US/60/278,983
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; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark
; APPLICANT: Gwynne, David
; TITLE OF INVENTION: Methods for Treating Muscle Diseases and
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 04585/028001
; CURRENT APPLICATION NUMBER: US/08/209,204D
; CURRENT FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: US 08/059,022
; PRIOR FILING DATE: 1993-05-06
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-209-204D-40

Query Match          100.0%; Score 69; DB 6; Length 39;
Best Local Similarity 10.8%; Pred. No. 3.4e+03;
Matches      4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
US-08-209-204E-40
; Sequence 40, Application US/08209204E
; GENERAL INFORMATION:
; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark
; APPLICANT: Gwynne, David
; TITLE OF INVENTION: Methods for Treating Muscle Diseases and
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 04585/028001
; CURRENT APPLICATION NUMBER: US/08/209,204E
; CURRENT FILING DATE: 1994-03-08
; PRIOR APPLICATION NUMBER: US 08/059,022
; PRIOR FILING DATE: 1993-05-06
; NUMBER OF SEQ ID NOS: 420
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-209-204E-40

Query Match          100.0%; Score 69; DB 6; Length 39;
Best Local Similarity 10.8%; Pred. No. 3.4e+03;
Matches      4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

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DB    3 CGCKCRRITTCACRCAAGGTTCTTCTCTCTCAGC 39

RESULT 12
US-08-461-097-40
; Sequence 40, Application US/08461097
; GENERAL INFORMATION:
; APPLICANT: Robert Sklar, Mark Marchionni,
; APPLICANT: David I. Gwynne
; TITLE OF INVENTION: METHODS FOR TREATING
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2005, 00:32:31 ; Search time 52 Seconds
(without alignments)
81.197 Million cell updates/sec

Title: US-09-763-616-2

Perfect score: 69
Sequence: 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXC 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 537409 seqs, 114114291 residues

Total number of hits satisfying chosen parameters: 537409

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New *

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	69	100.0	55	7	US-11-097-143-26459
3	69	100.0	56	7	US-11-097-143-26490
4	69	100.0	59	6	US-10-526-324-658
5	69	100.0	61	6	US-10-450-763-53958
6	69	100.0	63	7	US-11-097-143-26472
7	69	100.0	66	8	US-60-669-241-25327
8	69	100.0	71	7	US-11-079-463-9113
9	69	100.0	71	7	US-11-079-045-9113
10	69	100.0	72	7	US-11-097-143-26460
11	69	100.0	74	7	US-11-097-143-26457
12	69	100.0	76	6	US-10-703-032-107111
13	69	100.0	76	6	US-10-703-032-192031
14	69	100.0	80	8	US-60-669-175-32704
15	69	100.0	84	6	US-10-467-657-5372
16	69	100.0	84	6	US-10-467-657A-5372
17	69	100.0	87	6	US-10-450-763-53959
18	69	100.0	89	6	US-10-450-763-57805
19	69	100.0	92	6	US-10-703-032-164331
20	69	100.0	92	8	US-60-655-875-123185
21	69	100.0	92	8	US-60-655-875-160354
22	69	100.0	93	6	US-10-703-032-159412
23	69	100.0	93	6	US-10-703-032-192934
24	69	100.0	95	6	US-10-703-032-105601
25	69	100.0	97	6	US-10-530-253-29

26	69	100.0	97	6	US-10-703-032-141430	Sequence 141430,
27	69	100.0	98	1	PCT-US04-05292-6	Sequence 6, Appli
28	69	100.0	98	1	PCT-US04-13756-3	Sequence 3, Appli
29	69	100.0	98	1	PCT-US04-05292A-6	Sequence 6, Appli
30	69	100.0	98	6	US-10-530-253-14	Sequence 14, Appl
31	69	100.0	98	6	US-10-530-253-28	Sequence 28, Appl
32	69	100.0	98	6	US-10-530-253-36	Sequence 36, Appl
33	69	100.0	98	7	US-11-077-939-5	Sequence 5, Appli
34	69	100.0	98	8	US-60-655-875-134564	Sequence 134564,
35	69	100.0	98	8	US-60-655-875-168355	Sequence 168355,
36	69	100.0	98	8	US-60-655-875-170437	Sequence 170437,
37	69	100.0	99	1	PCT-US04-05292-5	Sequence 5, Appli
38	69	100.0	99	1	PCT-US04-05292-65	Sequence 65, Appl
39	69	100.0	99	1	PCT-US04-13756-2	Sequence 2, Appli
40	69	100.0	99	1	PCT-US04-05292A-5	Sequence 5, Appli
41	69	100.0	99	1	PCT-US04-05292A-65	Sequence 65, Appl
42	69	100.0	99	6	US-10-530-253-30	Sequence 30, Appl
43	69	100.0	99	6	US-10-530-253-34	Sequence 34, Appl
44	69	100.0	100	6	US-10-703-032-106880	Sequence 106880,
45	69	100.0	100	7	US-11-031-175-16481	Sequence 16481, A

ALIGNMENTS

RESULT 1
US-10-526-324-813

; SEQUENCE 813, Application US/10526324
; GENERAL INFORMATION:
; APPLICANT: Imanaka, Takayuki
; TITLE OF INVENTION: METHOD OF TARGETED GENE DISRUPTION, GENOME OF
; TITLE OF INVENTION: HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 490051.401USPC
; CURRENT APPLICATION NUMBER: US/10/526,324
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: PCT/IB2003/003597
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP 2002-319011
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2167
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 813
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Thermococcus kodakaraensis KOD1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (414542)..(414542)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (786890)..(786890)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (786907)..(786907)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (839139)..(839139)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1128488)..(1128488)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature

```
; LOCATION: (1128499)..(1128499)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1128505)..(1128506)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1128517)..(1128518)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1128539)..(1128540)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1561400)..(1561400)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1561477)..(1561477)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1561545)..(1561545)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1767941)..(1767941)
; OTHER INFORMATION: n is a or c or g or t.
US-10-526-324-813
```

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Query Match 100.0%; Score 69; DB 6; Length 53;
Best Local Similarity 10.8%; Pred. No. 1.2e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 6 CIVCGYIDEDEGDPDSGIAPTKAFEDLPDWVCPLC 42
```

```
RESULT 2
US-11-097-143-26469
; Sequence 26469, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26469
; LENGTH: 55
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```
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26469

Query Match 100.0%; Score 69; DB 7; Length 55;
Best Local Similarity 10.8%; Pred. No. 1.3e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 3 CGPCGCGYCCGCGCGPCGCGPCGCGCGPCG 39

RESULT 3
US-11-097-143-26490
; Sequence 26490, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26490
; LENGTH: 56
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26490

Query Match 100.0%; Score 69; DB 7; Length 56;
Best Local Similarity 10.8%; Pred. No. 1.3e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 10 CGPCGCGCGCGCGCGCGCGCGCGCGCGCG 46

RESULT 4
US-10-526-324-658
; Sequence 658, Application US/10526324
; GENERAL INFORMATION:
; APPLICANT: Imanaka, Takayuki
; APPLICANT: Atomi, Haruyuki
; TITLE OF INVENTION: METHOD OF TARGETED GENE DISRUPTION, GENOME OF
; TITLE OF INVENTION: HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 490051.401USPC
; CURRENT APPLICATION NUMBER: US/10/526,324
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: PCT/IB2003/003597
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP 2002-319011
```



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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26460
; LENGTH: 72
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26460

Query Match      100.0%; Score 69; DB 7; Length 72;
Best Local Similarity 10.8%; Pred. No. 1.8e+02;
Matches      4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY      1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
        |||:|||||:|||||:|||||:|||||:|||||:
Db      17 CGPCGCGGCGCGCGCGCGCGCGCGCGCGCGPC 53

RESULT 11
US-11-097-143-26457
; Sequence 26457, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26457
; LENGTH: 74
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26457

Query Match      100.0%; Score 69; DB 7; Length 74;
Best Local Similarity 10.8%; Pred. No. 1.9e+02;
Matches      4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

QY      1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
        |||:|||||:|||||:|||||:|||||:|||||:
Db      9 CGPCGCGGCGCGCGCGCGCGCGCGCGCGCGPC 45

RESULT 12
US-10-703-032-107111
; Sequence 107111, Application US/10703032
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Cao, Yongwei
; APPLICANT: Masucci, James D.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

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Fri May 27 09:41:02 2005

APPLICANT: Lu, Maolong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Wu, Wei
APPLICANT: Zhang, Bei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROL OF INSECT INFESTATION IN PLA
FILE REFERENCE: 38-21(53597)
CURRENT APPLICATION NUMBER: US/60/669,175
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60560842
PRIOR FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60565632
PRIOR FILING DATE: 2004-04-27
PRIOR APPLICATION NUMBER: 60579062
PRIOR FILING DATE: 2004-06-11
PRIOR APPLICATION NUMBER: 60603421
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60617261
PRIOR FILING DATE: 2004-10-11
NUMBER OF SEQ ID NOS: 40774
SEQ ID NO 32704
LENGTH: 80
TYPE: PRT
ORGANISM: Diabrotica virgifera

FEATURE:
OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_12401; Strand=-; Position=59
US-60-669-175-32704

Query Match 100.0%; Score 69; DB 8; Length 80;
Best Local Similarity 10.8%; Pred. No. 2.1e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 21 CVVCAKSLQYTKLYNPSYVEWIIINLFLSGVCRGC 57

RESULT 15

US-10-467-657-5372
Sequence 5372, Application US/10467657
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 5372
LENGTH: 84
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5372

Query Match 100.0%; Score 69; DB 6; Length 84;
Best Local Similarity 10.8%; Pred. No. 2.3e+02;
Matches 4; Conservative 33; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXC 37
Db 34 CPGCWIYDELGDEHGIAFGTKFEDIPDDWKCEC 70

Search completed: May 27, 2005, 00:46:14
Job time : 53 secs